Amendments to the Claims:

1. (Currently Amended) A method for determining ~~mutation load~~ the frequency or nature of mutations in a cell sample, which comprises identifying a single somatic cell in said sample that contains ~~accumulated levels of~~ p53 protein accumulated by missense mutations in exons 5 through 9, amplifying by PCR a DNA molecule of said identified single somatic cell which is at least 1 kb in size and which spans exons 5 to 9 of p53 to produce a PCR product, and determining the frequency or nature of mutations in said amplified ~~DNA~~ PCR product.

2-4 (Canceled herein).

5. (Currently Amended) The method of claim 1, in which said single somatic cell is identified by immunohistochemical staining for p53.

6-9. (Canceled herein).

10. (Currently Amended) The method of claim ~~8~~ 1, wherein said DNA molecule is at least 2 kb in size.

11. (Currently Amended) The method of claim ~~7~~ 27, in which said carrier DNA is mouse DNA that has an average size of at least ~~about~~ 20 kb.

12. (Currently Amended) The method of claim 1, in which ~~the method is performed on a~~ said single somatic cell ~~which~~ is obtained by microdissection from a paraffin-embedded tissue section.

13. (Previously presented) The method of claim 12, in which said tissue section is fixed with ethanol.

14. (Previously presented) The method of claim 12 in which said tissue section is subjected to steam heating in the presence of EDTA.

15. (Currently Amended) The method of claim 1, in which ~~the~~ said amplification ~~step~~ is performed using two different DNA polymerases.

16-17. (Canceled).

18. (Currently Amended) The method of claim ~~11~~ 27, in which said amplification is performed using primers GCCGTCTTCCAGTTGCTTTATCTGTTCACT (SEQ. ID. NO. 1) and CCTGATGGCAAATGCCCCAATTGCAGGTAA (SEQ. ID. NO. 2).

19. (Currently Amended) The method of claim ~~11~~ 27, in which said amplification is performed using primers GCCGTCTTCCAGTTGCTTTATCTGTTCACT (SEQ. ID. NO. 1) and GTCAAGTAGCATCTGTATCAGGCAAAGTCATAG (SEQ. ID. NO. 3).

20. (Original) The method of claim 12, in which the paraffin-embedded tissue section is prepared from a sample that originated from a patient that is at risk for developing a cancerous condition.

21. (Original) The method of claim 12, in which the paraffin-embedded tissue section is prepared from a sample that originated from a patient that is currently receiving treatment for a present cancer condition.

22. (Original) The method of claim 21, in the treatment is radiation treatment.

23. (Original) The method of claim 21, in the treatment is cytotoxic drug treatment.

24. (Original) The method of claim 21, in the treatment is gene therapy treatment.

25. (Currently Amended) The method of claim ~~1~~ 27, in which the frequency or nature of mutations is determined by sequence analysis using a primer selected from the group consisting of TGCCCTGACTTTCAACTCTGTCTC (SEQ. ID. NO. 5), AGGGTCCCCAGGCCTCTGAT (SEQ. ID. NO. 6), GGCCACTGACAACCACCCTTAA (SEQ. ID. NO. 7), AGGTCTCCCCAAGGCGCACT (SEQ. ID. NO. 8), GGGGCACAGCAGGCCAGTGT (SEQ. ID. NO. 9), GGAGAGACCGGCGCACAGA (SEQ. ID. NO. 10) and CGGCATTTTGAGTGTTAGACTGGA (SEQ. ID. NO. 11).

26. (Canceled).

27. (New) A method for determining the frequency of mutations in a single human somatic cell, which comprises:

(a) providing a paraffin-embedded tissue section containing human cells;

(b) identifying a single human somatic cell in said tissue section that contains p53 protein accumulated in said single somatic cell by missense mutations in exons 5 through 9 by immunohistochemical staining for p53;

(c) microdissecting said identified single human somatic cell from said tissue section;

(d) amplifying by PCR a p53 DNA sequence of said identified single somatic cell in the presence of carrier DNA using two different polymerases, wherein said DNA sequence is at least 1 kb in size and spans exons 5 to 9 of p53, to form a PCR product of at least 1 kb in size; and

(e) determining the frequency or nature of mutations in said PCR product by sequence analysis of said PCR product.